O2 80

0400 #2

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RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,549 TIME: 10:11:22

Input Set : A:\3534107u.app
Output Set: N:\CRF3\12142001\I005549.raw

ENTERED

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 3 <110> APPLICANT: BOWEN, MICHAEL A.
 4        WU, YULI
 5        YANG, WEN-PIN
 6        FINGER, JOSHUA
 7        NADLER, STEVEN
 8        CARROLL, PAMELA
 9        FEDER, JOHN
11 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING AN ACTIVATED HUMAN
12        T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN
13        CONJUGATING ENZYME
15 <130> FILE REFERENCE: D0034np
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C--> 17 **<140> CURRENT APPLICATION NUMBER: US/10/005,549**
C--> 18 **<141> CURRENT FILING DATE: 2001-10-29**

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20 <150> PRIOR APPLICATION NUMBER: 60/308,706
21 <151> PRIOR FILING DATE: 2001-07-30
23 <150> PRIOR APPLICATION NUMBER: 60/244,688
24 <151> PRIOR FILING DATE: 2000-10-30
26 <160> NUMBER OF SEQ ID NOS: 55
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2254
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (517)..(1782)
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44 ccctctccgg ccccggccgg ggggcgggcg ccggcggctt tggtgactct agataacctc 180
46 gggccgatcg cacgccccccc gtggcggcga cgacccattc gaacgtctgc cctatcaact 240
48 ttcgatggta gtcgccgtgc ctaccatggt gaccacgggt gacggggaat cagggttcga 300
50 ttccggagag ggagcctgag aaacggctac cacatccaag gaaggcagca ggcgcgcaaa 360
52 ttacccactc ccggaggtgg cggcggcgcc atcttggcga agggggggatc aggaagtgcg 420
54 gaccgcggcg gcggcggcgg cggcggcggc ggcggagccc ggagcgcagg ccggaggctc 480
56 ccggcccgcc ggccccggag cggagcggag cggagg atg cag cag ccg cag ccg    534
57                                          Met Gln Gln Pro Gln Pro
58                                           1               5
60 cag ggg cag cag cag ccg ggg ccg ggg cag cag ctg ggg ggc cag ggg   582
61 Gln Gly Gln Gln Gln Pro Gly Pro Gly Gln Gln Leu Gly Gly Gln Gly
62             10              15                  20
64 gcg gcg ccg ggg gcc ggg ggc ggc cca ggg ggg ggc ccg ggg ccg ggg   630
65 Ala Ala Pro Gly Ala Gly Gly Gly Pro Gly Gly Gly Pro Gly Pro Gly
66             25              30                  35
68 ccc tgc ctg agg cga gag ctg aag ctg ctc gag tcc atc ttc cac cgc   678
69 Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu Glu Ser Ile Phe His Arg
70     40              45                  50
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72 ggc cac gag cgc ttc cgc att gcc agc gcc tgc ctg gac gag ctg agc    726
73 Gly His Glu Arg Phe Arg Ile Ala Ser Ala Cys Leu Asp Glu Leu Ser
74  55                    60                  65                  70
76 tgc gag ttc ctg ctg gct ggg gcc gga ggg gcc ggg gcg ggg gcc gcg    774
77 Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly Ala Gly Ala Gly Ala Ala
78                      75                  80                  85
80 ccc gga ccg cat ctc ccc cca cgg ggg tcg gtg cct ggg gat cct gtc    822
81 Pro Gly Pro His Leu Pro Pro Arg Gly Ser Val Pro Gly Asp Pro Val
82                      90                  95                 100
84 cgc atc cac tgc aac atc acg gag tca tac cct gct gtg ccc ccc atc    870
85 Arg Ile His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro Ile
86             105                 110                 115
88 tgg tcg gtg gag tct gat gac cct aac ttg gct gct gtc ttg gag agg    918
89 Trp Ser Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu Arg
90     120                 125                 130
92 ctg gtg gac ata aag aaa ggg aat act ctg cta ttg cag cat ctg aag    966
93 Leu Val Asp Ile Lys Lys Gly Asn Thr Leu Leu Leu Gln His Leu Lys
94 135                 140                 145                 150
96 agg atc atc tcc gac ctg tgt aaa ctc tat aac ctc cct cag cat cca   1014
97 Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr Asn Leu Pro Gln His Pro
98                 155                 160                 165
100 gat gtg gag atg ctg gat caa ccc ttg cca gca gag cag tgc aca cag   1062
101 Asp Val Glu Met Leu Asp Gln Pro Leu Pro Ala Glu Gln Cys Thr Gln
102             170                 175                 180
104 gaa gac gtg tct tca gaa gat gaa gat gag gag atg cct gag gac aca   1110
105 Glu Asp Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp Thr
106             185                 190                 195
108 gaa gac tta gat cac tat gaa atg aaa gag gaa gag cca gct gag ggc   1158
109 Glu Asp Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu Gly
110     200                 205                 210
112 aag aaa tct gaa gat gat ggc att gga aaa gaa aac ttg gcc atc cta   1206
113 Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile Leu
114 215                 220                 225                 230
116 gag aaa att aaa aag aac cag agg caa gat tac tta aat ggt gca gtg   1254
117 Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala Val
118                 235                 240                 245
120 tct ggc tcg gtg cag gcc act gac cgg ctg atg aag gag ctc agg gat   1302
121 Ser Gly Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Arg Asp
122             250                 255                 260
124 ata tac cga tca cag agt ttc aaa ggc gga aac tat gca gtc gaa ctc   1350
125 Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly Asn Tyr Ala Val Glu Leu
126             265                 270                 275
128 gtg aat gac agt ctg tat gat tgg aat gtc aaa ctc ctc aaa gtt gac   1398
129 Val Asn Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu Leu Lys Val Asp
130     280                 285                 290
132 cag gac agc gct ttg cac aac gat ctc cag atc ctc aaa gag aaa gaa   1446
133 Gln Asp Ser Ala Leu His Asn Asp Leu Gln Ile Leu Lys Glu Lys Glu
134 295                 300                 305                 310
136 gga gcc gac ttc att cta ctt aac ttt tcc ttt aaa gat aac ttt ccc   1494
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137 Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro
138             315                 320                 325
140 ttt gac cca cca ttt gtc agg gtt gtg tct cca gtc ctc tct gga ggg 1542
141 Phe Asp Pro Pro Phe Val Arg Val Val Ser Pro Val Leu Ser Gly Gly
142             330                 335                 340
144 tat gtt ctg ggc gga ggg gcc atc tgc atg gaa ctt ctc acc aaa cag 1590
145 Tyr Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr Lys Gln
146             345                 350                 355
148 ggc tgg agc agt gcc tac tcc ata gag tca gtg atc atg cag atc agt 1638
149 Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Val Ile Met Gln Ile Ser
150             360                 365                 370
152 gcc aca ctg gtg aag ggg aaa gca cga gtg cag ttt gga gcc aac aaa 1686
153 Ala Thr Leu Val Lys Gly Lys Ala Arg Val Gln Phe Gly Ala Asn Lys
154 375             380                 385                 390
156 tct caa tac agt ctg aca aga gca cag cag tcc tac aag tcc ttg gtg 1734
157 Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln Ser Tyr Lys Ser Leu Val
158             395                 400                 405
160 cag atc cac gaa aaa aac ggc tgg tac aca ccc cca aaa gaa gac ggc 1782
161 Gln Ile His Glu Lys Asn Gly Trp Tyr Thr Pro Pro Lys Glu Asp Gly
162             410                 415                 420
164 taaccctgga gtatcaccct tcctccctcc ccaggcacca ctggaccaat tacctttgaa 1842
166 tgctgtattt ggatctcacg ctgcctctgt ggttccctcc ctcatttttc ctggacgtga 1902
168 tagctctgcc tattgcagga caatgatggc tattctaaac gctaaggaaa aaaaacaaac 1962
170 acagaactgt ttcaagtact caagactgac ttacagacca accaaccacc ttgctggaac 2022
172 ccttgctagc aggcattctt ataaagaaa ctttcgagcc tccttatatt gctggaaact 2082
174 cagctgtgct ccagactaga gcctccttac ctatgctatg gattttttaat ttattttctc 2142
176 ttatttcatg tacactgctt tttttggtta cagtgtatga tggatgtgta tgaaaaaaat 2202
178 gtatctttgg gaaaacaatt acagtttgtt aatttgaaaa aaaaaaaaaa aa         2254
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182 <211> LENGTH: 422
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
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188  1               5                 10                  15
190 Gln Leu Gly Gly Gln Gly Ala Ala Pro Gly Ala Gly Gly Gly Pro Gly
191             20                  25                  30
193 Gly Gly Pro Gly Pro Gly Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu
194             35                  40                  45
196 Glu Ser Ile Phe His Arg Gly His Glu Arg Phe Arg Ile Ala Ser Ala
197     50                  55                  60
199 Cys Leu Asp Glu Leu Ser Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly
200 65                  70                  75                  80
202 Ala Gly Ala Gly Ala Ala Pro Gly Pro His Leu Pro Pro Arg Gly Ser
203             85                  90                  95
205 Val Pro Gly Asp Pro Val Arg Ile His Cys Asn Ile Thr Glu Ser Tyr
206             100                 105                 110
208 Pro Ala Val Pro Pro Ile Trp Ser Val Glu Ser Asp Asp Pro Asn Leu
209             115                 120                 125
```

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211 Ala Ala Val Leu Glu Arg Leu Val Asp Ile Lys Lys Gly Asn Thr Leu
212     130             135             140
214 Leu Leu Gln His Leu Lys Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr
215 145             150             155             160
217 Asn Leu Pro Gln His Pro Asp Val Glu Met Leu Asp Gln Pro Leu Pro
218             165             170             175
220 Ala Glu Gln Cys Thr Gln Glu Asp Val Ser Ser Glu Asp Glu Asp Glu
221             180             185             190
223 Glu Met Pro Glu Asp Thr Glu Asp Leu Asp His Tyr Glu Met Lys Glu
224         195             200             205
226 Glu Glu Pro Ala Glu Gly Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys
227         210             215             220
229 Glu Asn Leu Ala Ile Leu Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp
230 225             230             235             240
232 Tyr Leu Asn Gly Ala Val Ser Gly Ser Val Gln Ala Thr Asp Arg Leu
233             245             250             255
235 Met Lys Glu Leu Arg Asp Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly
236         260             265             270
238 Asn Tyr Ala Val Glu Leu Val Asn Asp Ser Leu Tyr Asp Trp Asn Val
239         275             280             285
241 Lys Leu Leu Lys Val Asp Gln Asp Ser Ala Leu His Asn Asp Leu Gln
242         290             295             300
244 Ile Leu Lys Glu Lys Glu Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser
245 305             310             315             320
247 Phe Lys Asp Asn Phe Pro Phe Asp Pro Pro Phe Val Arg Val Val Ser
248             325             330             335
250 Pro Val Leu Ser Gly Gly Tyr Val Leu Gly Gly Gly Ala Ile Cys Met
251         340             345             350
253 Glu Leu Leu Thr Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser
254         355             360             365
256 Val Ile Met Gln Ile Ser Ala Thr Leu Val Lys Gly Lys Ala Arg Val
257     370             375             380
259 Gln Phe Gly Ala Asn Lys Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln
260 385             390             395             400
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265 Pro Pro Lys Glu Asp Gly
266             420
269 <210> SEQ ID NO: 3
270 <211> LENGTH: 471
271 <212> TYPE: PRT
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279             20              25              30
281 Asp Glu Leu Ser Met Lys Phe Ile Asn Ala Glu Asn Lys Gly Ile Ile
282         35              40              45
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284 Val Thr Ala Asn Ile Gln Glu Asn Tyr Pro Arg Gln Pro Pro Ile Trp
285     50                  55                  60
287 Phe Ser Glu Ser Asp Asp Val Pro Val Ile Gly Met Ser Leu Gln Arg
288 65                  70                  75                  80
290 Leu Thr Glu Thr Glu Glu Ser Thr Asn Ile Leu His Gln Val His Arg
291                 85                  90                  95
293 Leu Val Ser Asp Leu Cys Ser Phe Tyr Asn Leu Gln Met Pro Cys Glu
294             100                 105                 110
296 Leu Pro Gln Ile Ala Pro Pro Val Arg Asp Asp Ile Asp Glu Gly Arg
297         115                 120                 125
299 Gly Ser Asp Ile Ser Asp Thr Thr Ser Glu Pro Ile Asp Asp Asp Met
300     130                 135                 140
302 Ala Gly Asp Gly Glu Val Asp Asp Asp Glu Glu Glu Glu Asp Asp
303 145                 150                 155                 160
305 Glu Asp Ala Asp Gly Asp Ile Glu Ile Val Glu Met Ala Glu Glu Asp
306             165                 170                 175
308 Pro Thr Ser Gln His Asp Val Gly Val Ser Lys Glu Gly Leu Asp Met
309             180                 185                 190
311 Leu Asp Lys Val Ser Lys Ile Asn Arg Gln Gln His Leu Asp Gly Lys
312         195                 200                 205
314 Val Gln Gly Ser Ile Thr Ala Thr Asp Arg Leu Met Lys Glu Ile Arg
315     210                 215                 220
317 Asp Ile His Arg Ser Glu His Phe Lys Asn Gly Ile Tyr Thr Phe Glu
318 225                 230                 235                 240
320 Leu Glu Lys Glu Glu Asn Leu Tyr Gln Trp Trp Ile Lys Leu His Lys
321             245                 250                 255
323 Val Asp Glu Asp Ser Pro Leu Phe Glu Asp Met Lys Lys Leu Lys Lys
324             260                 265                 270
326 Asp His Asn Gln Asp His Leu Leu Phe Ser Phe Thr Phe Asn Glu Lys
327         275                 280                 285
329 Phe Pro Cys Asp Pro Pro Phe Val Arg Val Val Ala Pro His Ile Asn
330     290                 295                 300
332 Gln Gly Phe Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr
333 305                 310                 315                 320
335 Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Cys Ile Leu Gln
336             325                 330                 335
338 Ile Ala Ala Thr Leu Val Lys Gly Arg Ala Arg Ile Ser Phe Asp Ala
339             340                 345                 350
341 Lys His Thr Ser Thr Tyr Ser Met Ala Arg Ala Gln Gln Ser Phe Lys
342         355                 360                 365
344 Ser Leu Gln Gln Ile His Ala Lys Ser Gly Cys Thr Phe Leu Cys Ser
345     370                 375                 380
347 Thr Pro Ser Ser His Phe Phe Ala Leu His Leu Val Phe Phe Leu His
348 385                 390                 395                 400
350 Ser Asp Asp Phe Phe Phe Asn Gly Phe Leu Lys Ser Glu Thr Phe Thr
351             405                 410                 415
353 Phe Phe Lys Leu Ser Phe Arg Gly Tyr Ile Ser Ser Leu Val Leu Tyr
354         420                 425                 430
356 Ser Phe Ser Arg His Leu His His Pro Phe Phe Thr Arg Phe Leu Ile
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L:17 M:270 C: Current Application Number differs, Replaced Application Number
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date